Fig. 1

Strain KO11, Rice Hull Hydrolysate
(Tryptone and Yeast Extract)

Strain KO11, Rice Hull Hydrolysate
(Corn Steep Liquor)

Fig. 2

SSF with Office Paper and strain P2

Plot of Ethanol (g/L) versus Incubation time (h) showing curves labeled Original, Recycle 1, Recycle 2, and Recycle 3.

Fig. 3

EcoRI BamHI

celZ

Kan

pLOI2171
6.0 kbp

Rep (ts)

Fig. 4

Figure showing a scatter plot with a fitted line. The y-axis is labeled "Endoglucanase activity (IU/L)" ranging from 0 to 8000. The x-axis is labeled "Square of the radius of CMC zone (mm^2)" ranging from 0 to 70.

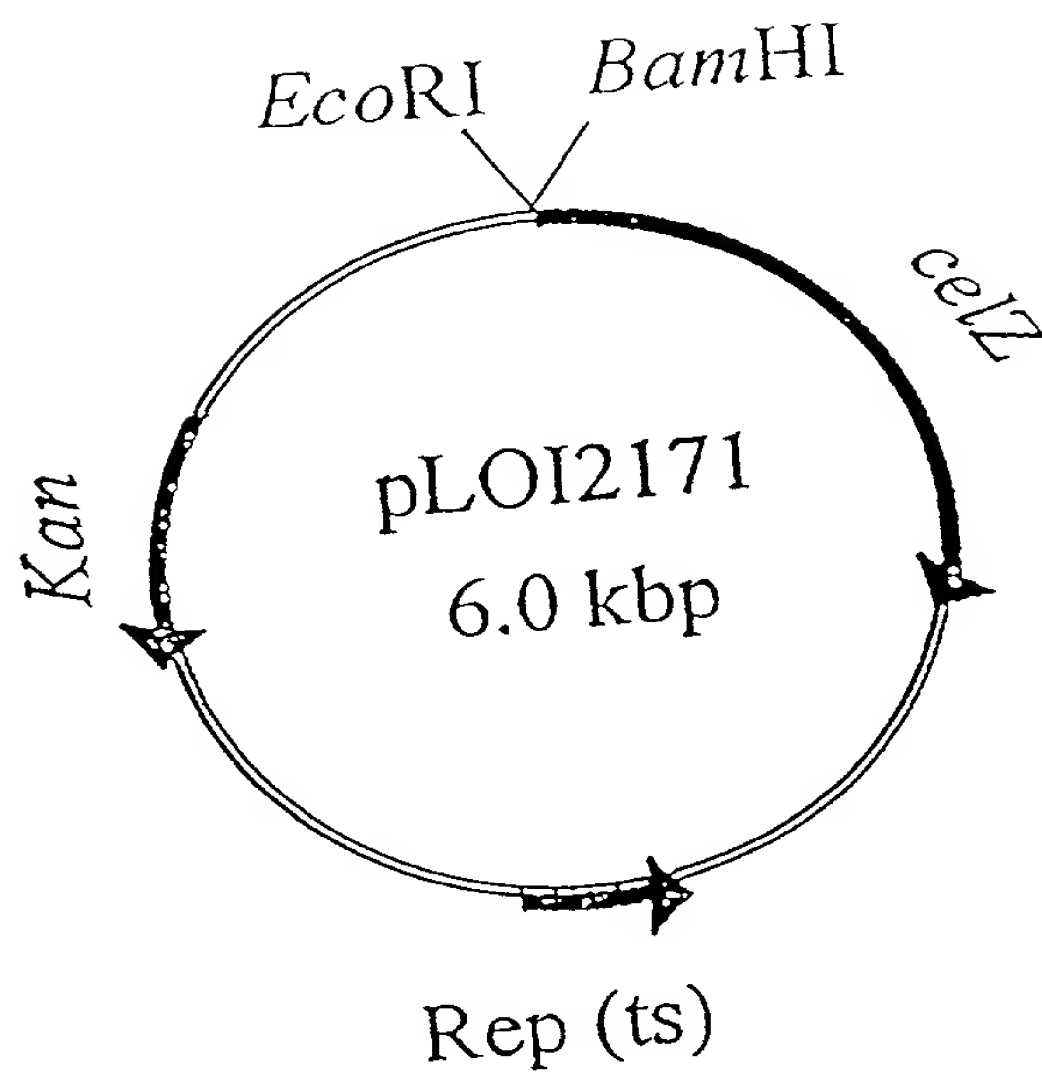**Fig. 5**

```
                 -35 region                              -10 region           #
1051 CTTTTTCGGC ATGAGCAACC AACATTTTCA AGGTATCATC CTGATGCGCA

1101 ATATCGGCAT CGGTTAGCCA TAACCATTTT ACCTGTCCGG CGGCCTTAAT
1151 ACCTTGATCA GATGGTTCGT GGTGTTGTTA CCTTGCCGAA GGGCACCGGT
1201 AAAAATGTTC GCGTCGGTGT TTTCGCCCGT GGCCCGAAAG CTGAAGAAGC
1251 TAAAGCTGCT GGTGCAGAAG TTGTCGGCGC AGAAGACCTG ATGGAAGCCA
                 -35 region                              -10 region
1301 TTCAGGGCGG CAGCATTGAT TTCGATCGTG ATGCCCTTTA TACTGAAATT

     #
1351 GCCTTGCGCT GCCATAATGA AGCAGCCTCC GGTGTTTTGG CAGATTTAAG

                                              Shine-Dalgarno
1401 CGCTGCCTGA TTTTCGTgat cctctagagt ctatgaaatg gagattcatt

     celZ coding region-->
1451 tatgcctctc tcttattcgg ataaccatcc agtcatccgc aagcttggcc
```
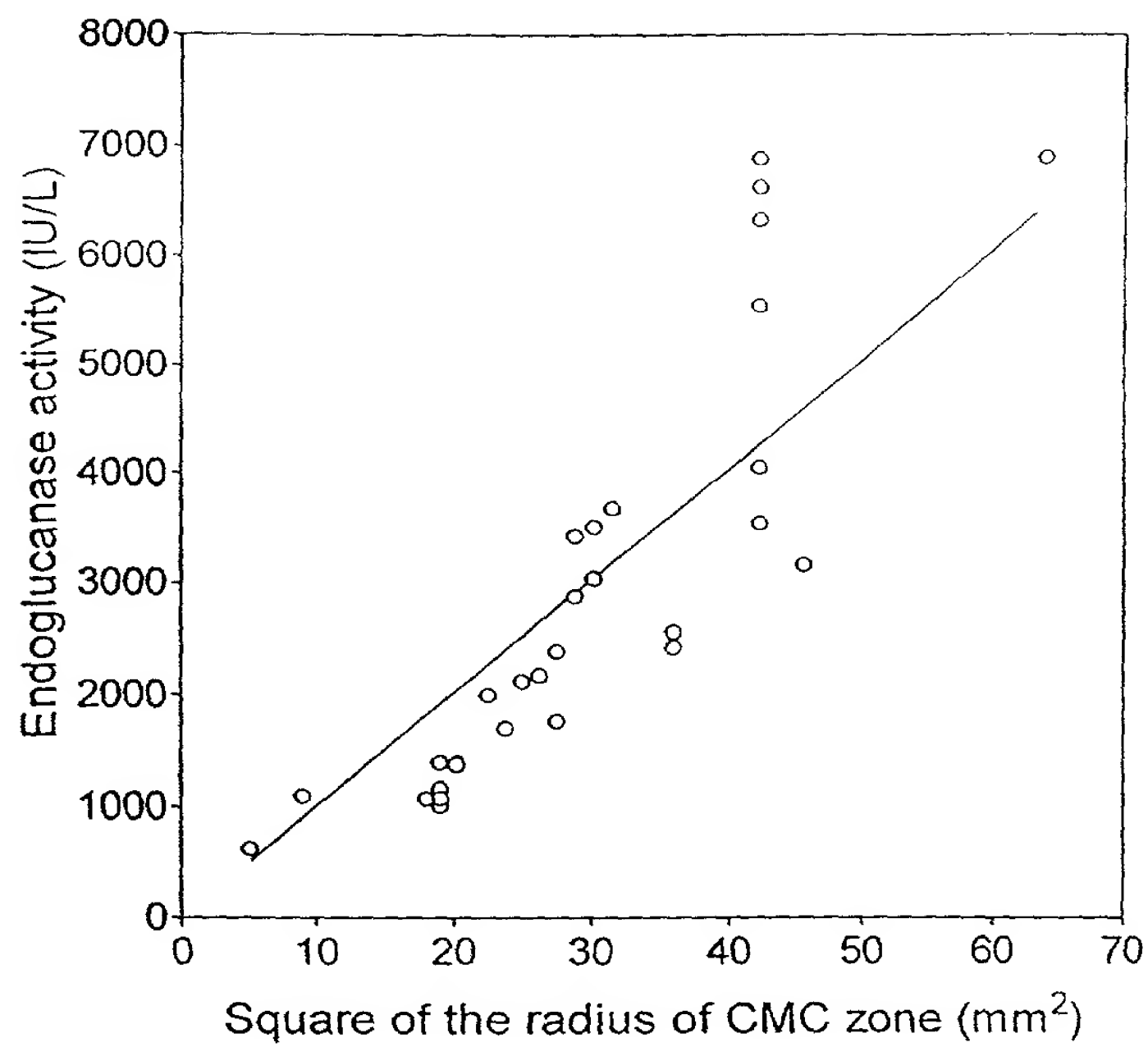
Fig. 6

Fig. 7

Fig. 8

Z. *mobilis* DNA

E. chrysanthemi DNA

Vector DNA

K. oxytoca DNA (target)

*Asc*I

*Asc*I

surrogate promoter

celZ

bla

tet

```
2000      4000      6000      8000      10000
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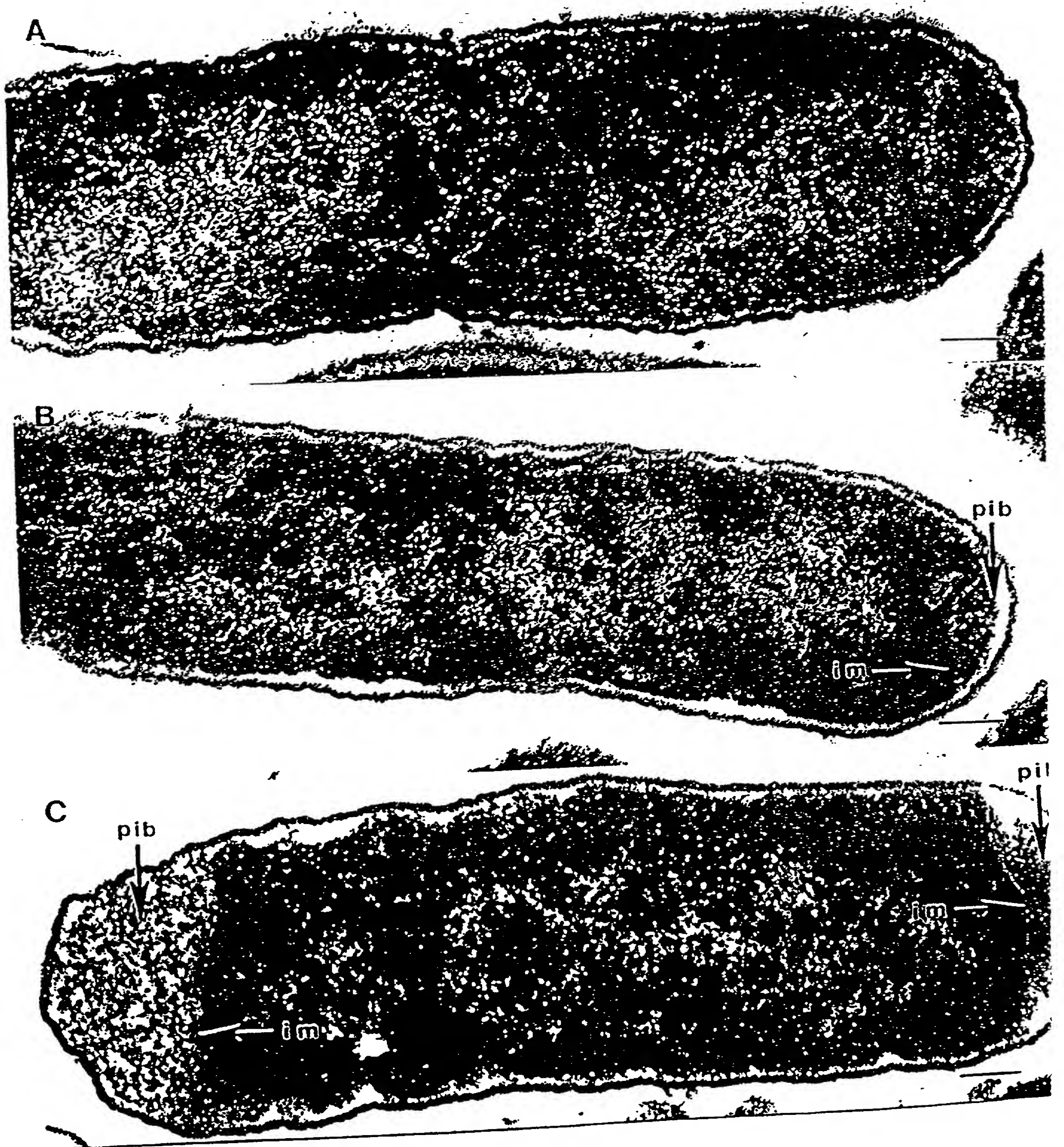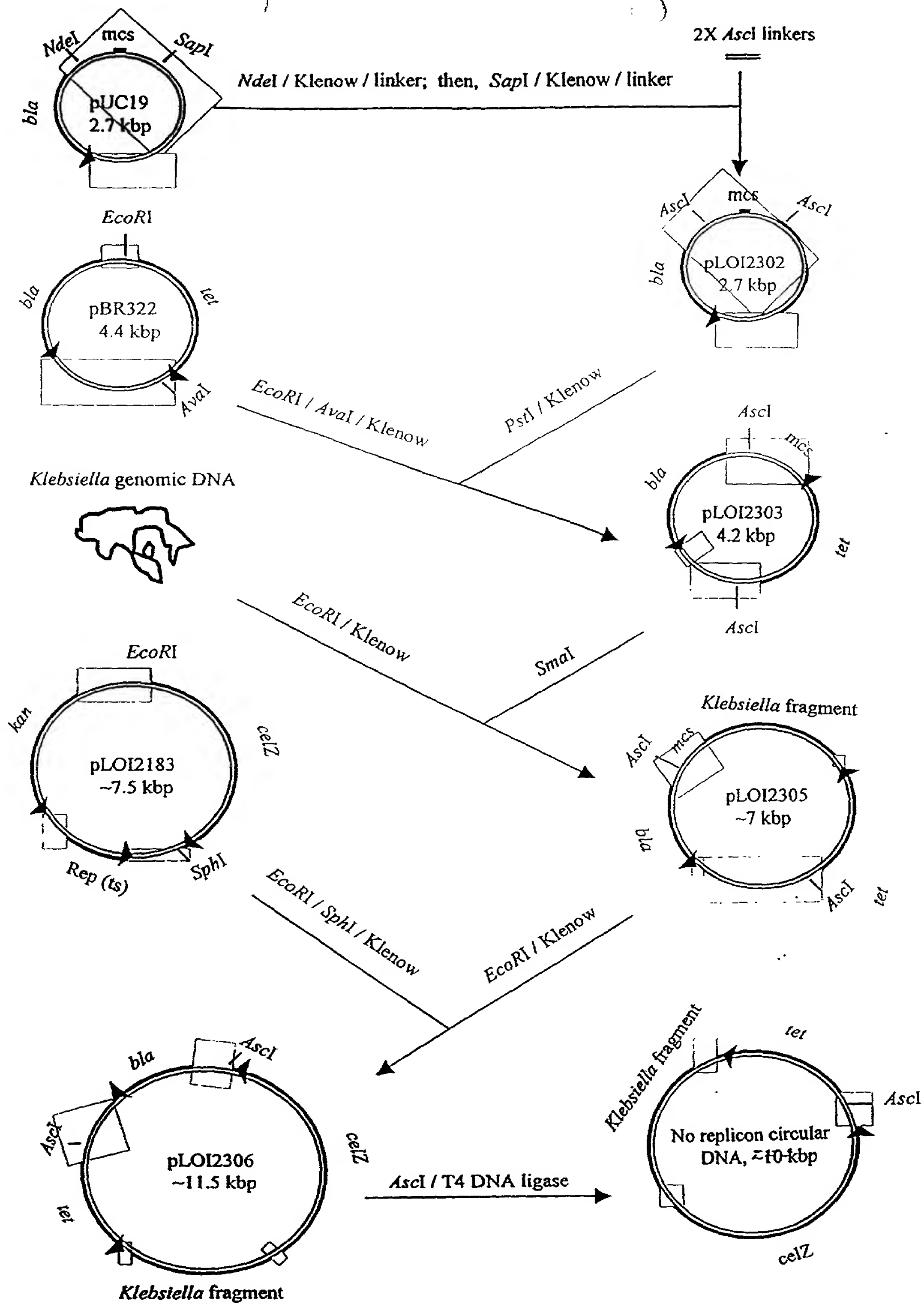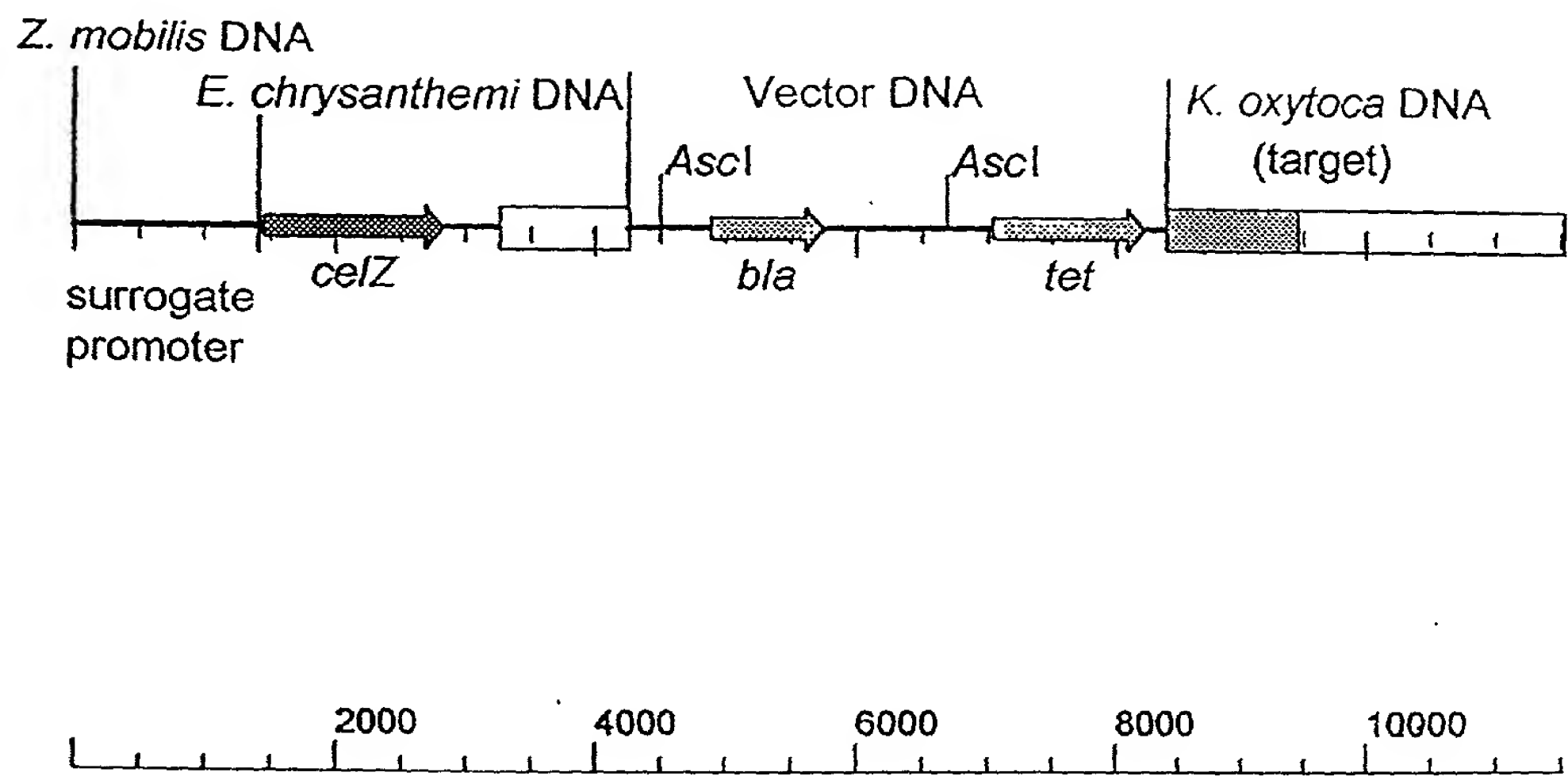
pLOI2306 (11520 bps)

Fig. 9

Fig. 10

Fig. 11

Fig. 12

= EGY

Δ = EGZ   Amorphous cellulose

Large fragments
~10 glucosyl units

Small fragments
< 6 glucosyl units

G-G   G-G-G

cellobiose & cellotriose

PTS Transporter

G-G-G-P & G-G-P

Cytoplasm

G-G-G-P & G-G-P

= phospho-β-glucosidase

Glycolysis
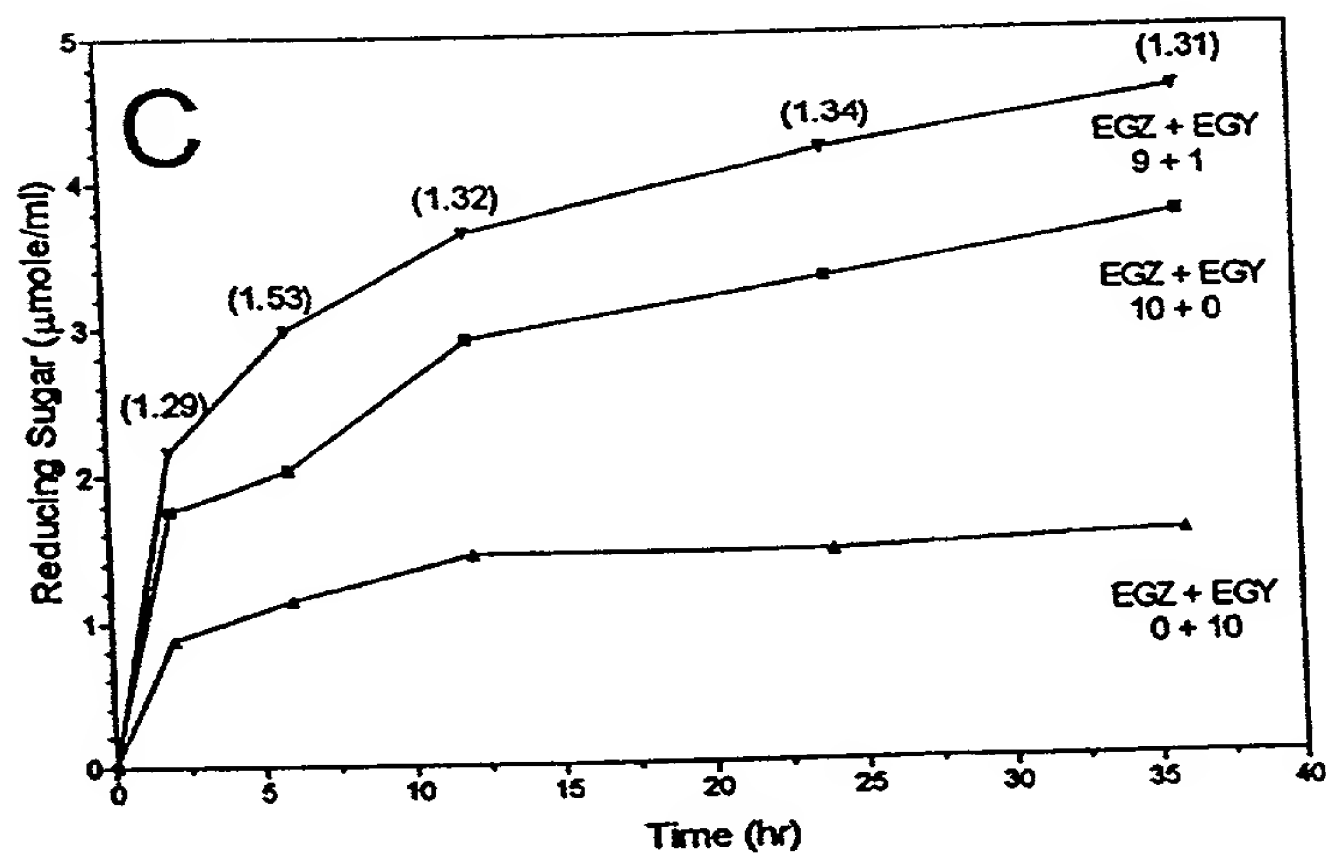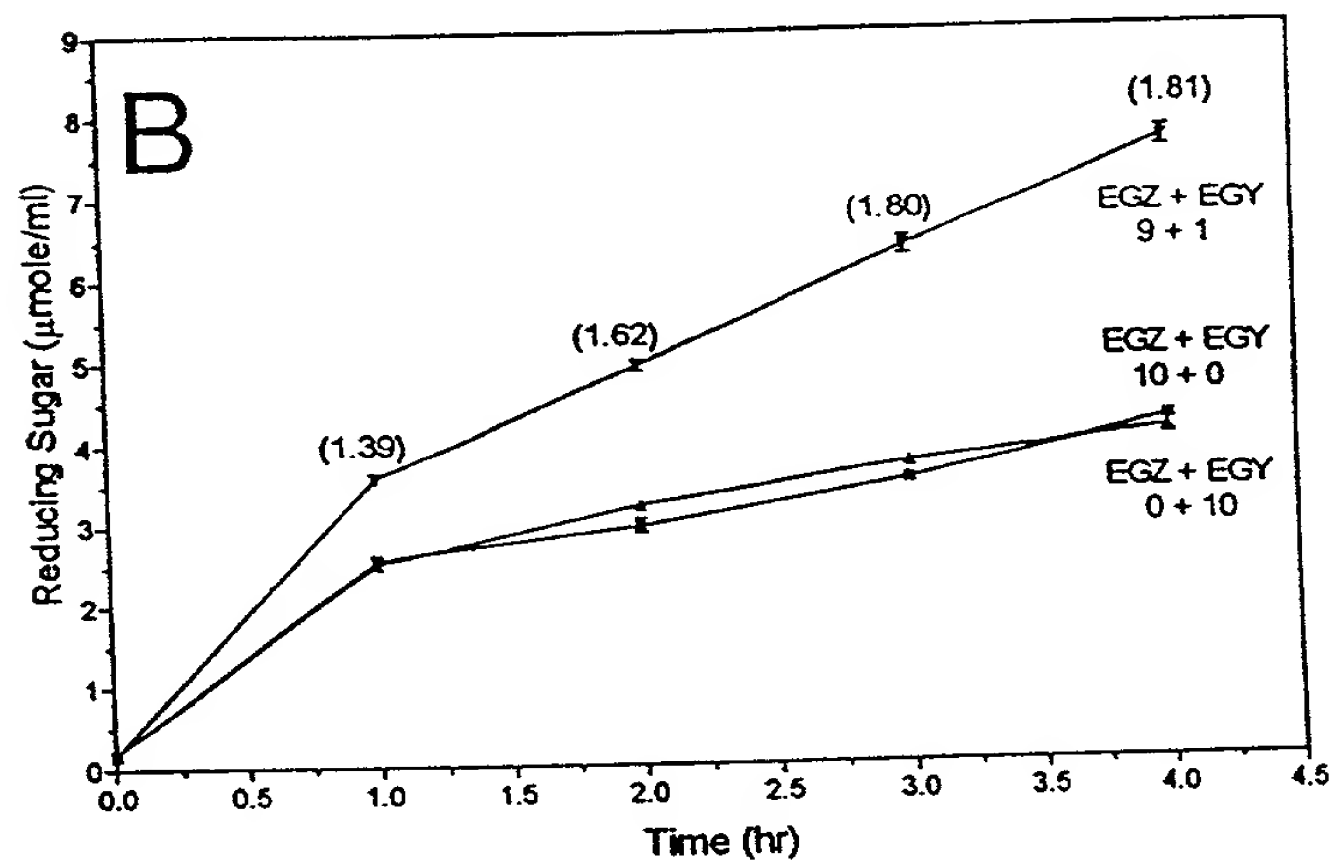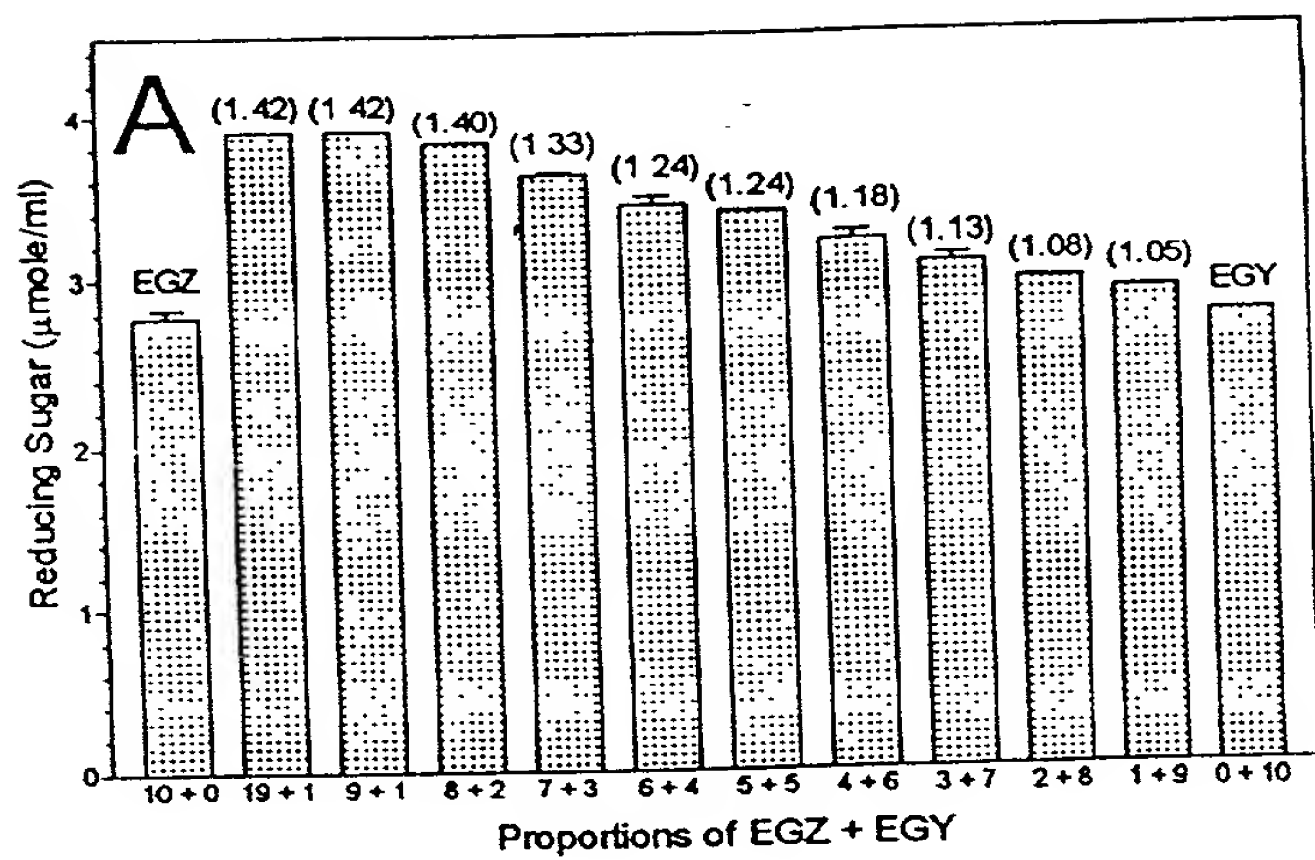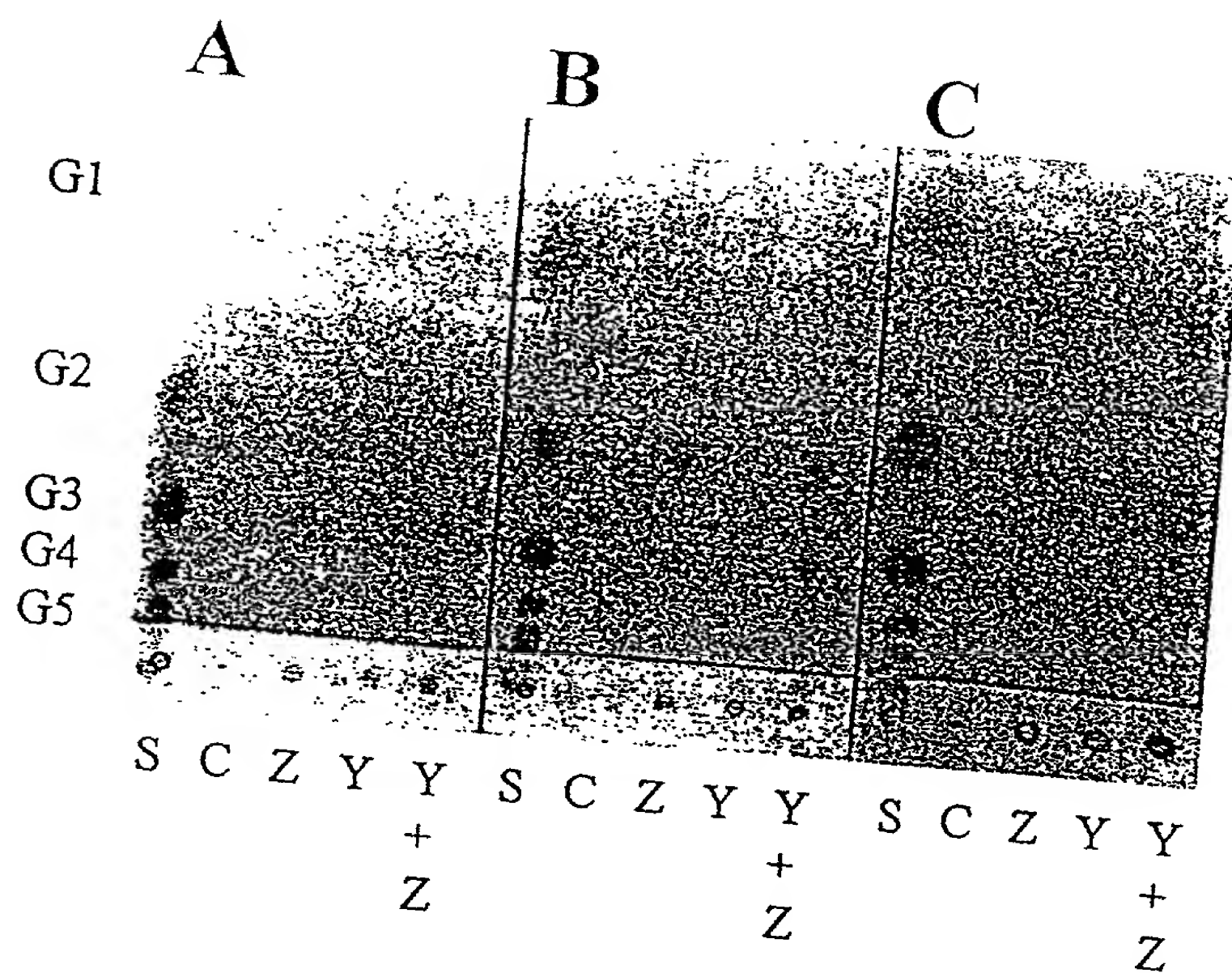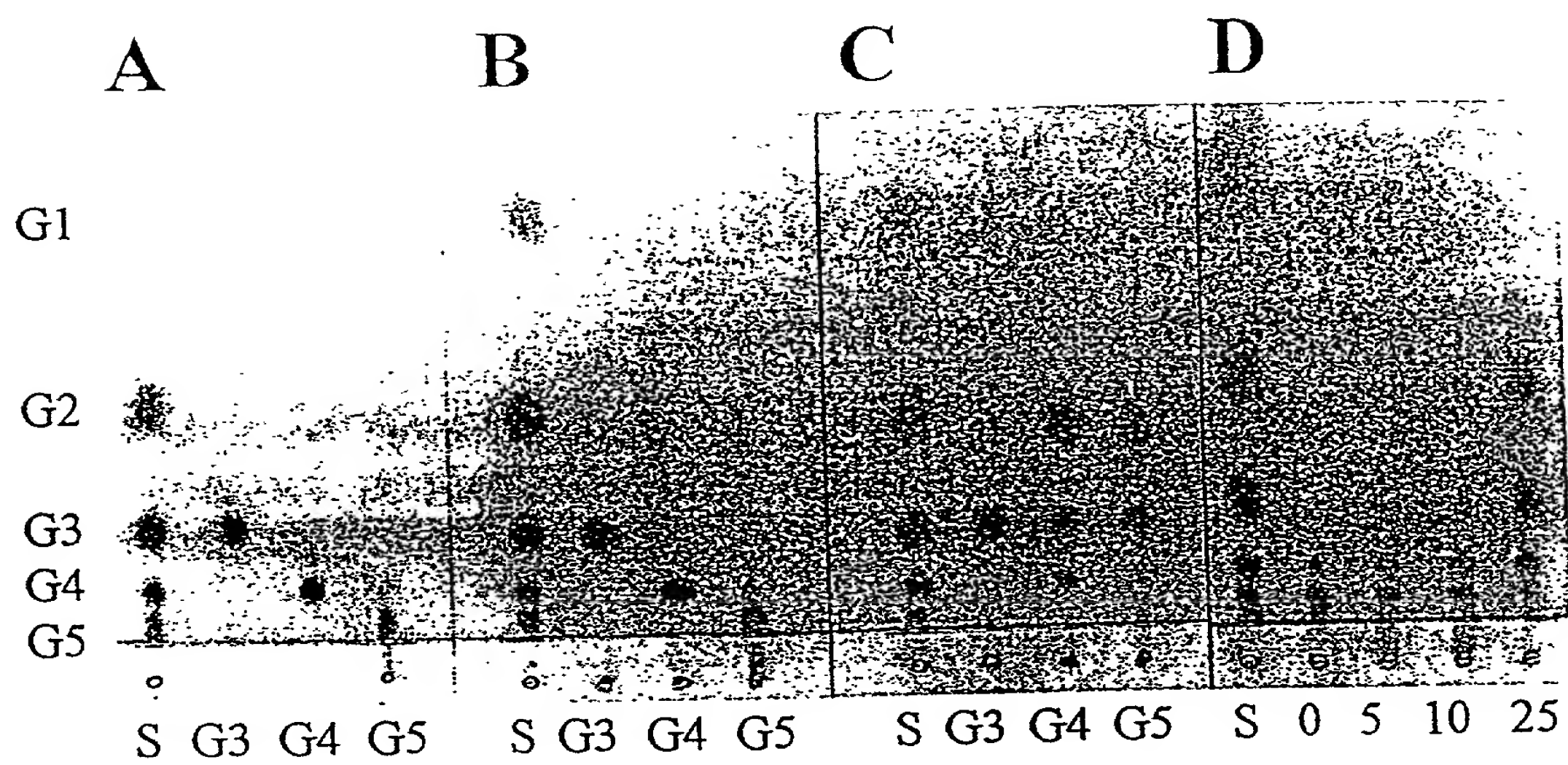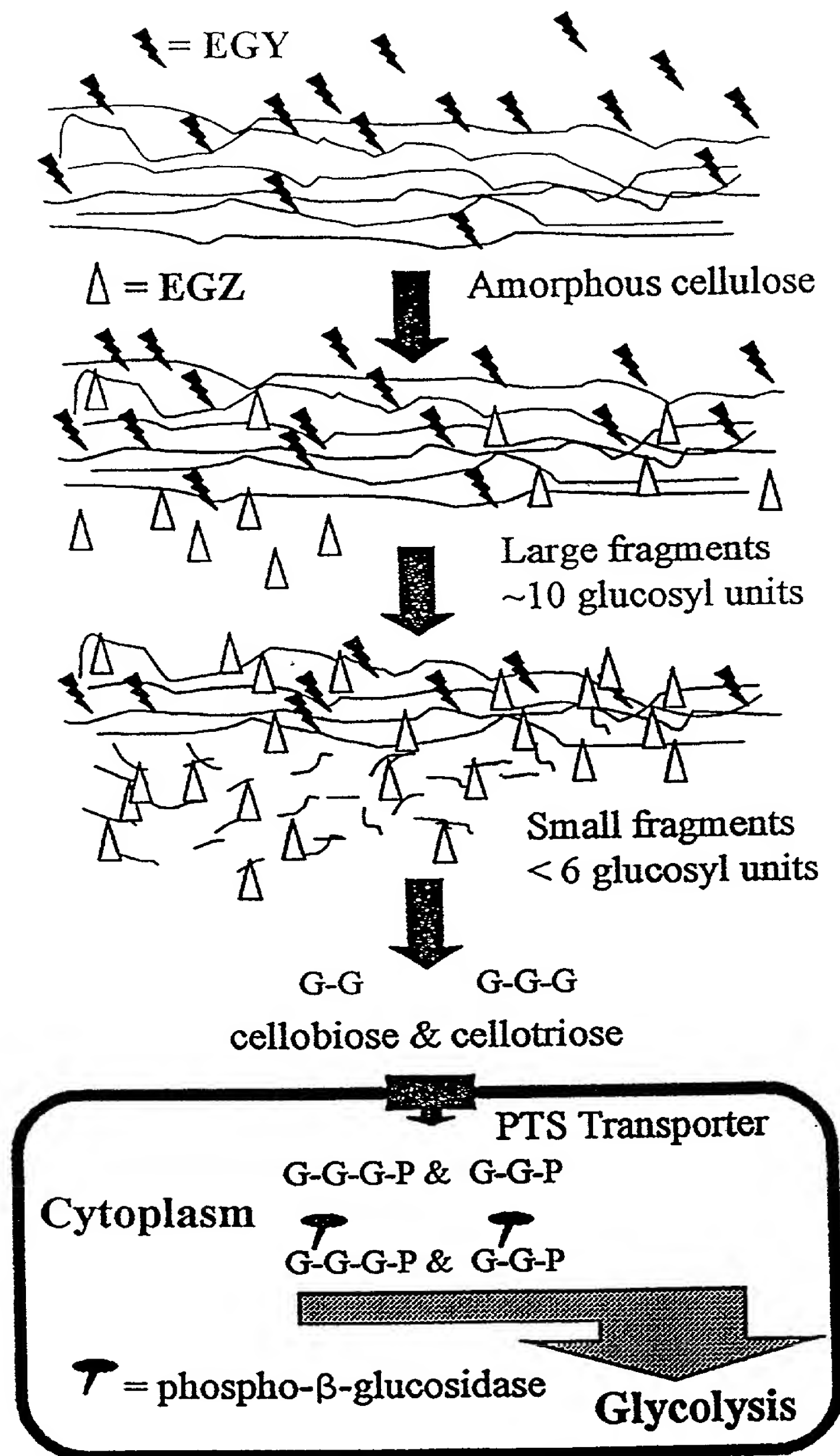
Fig. 13
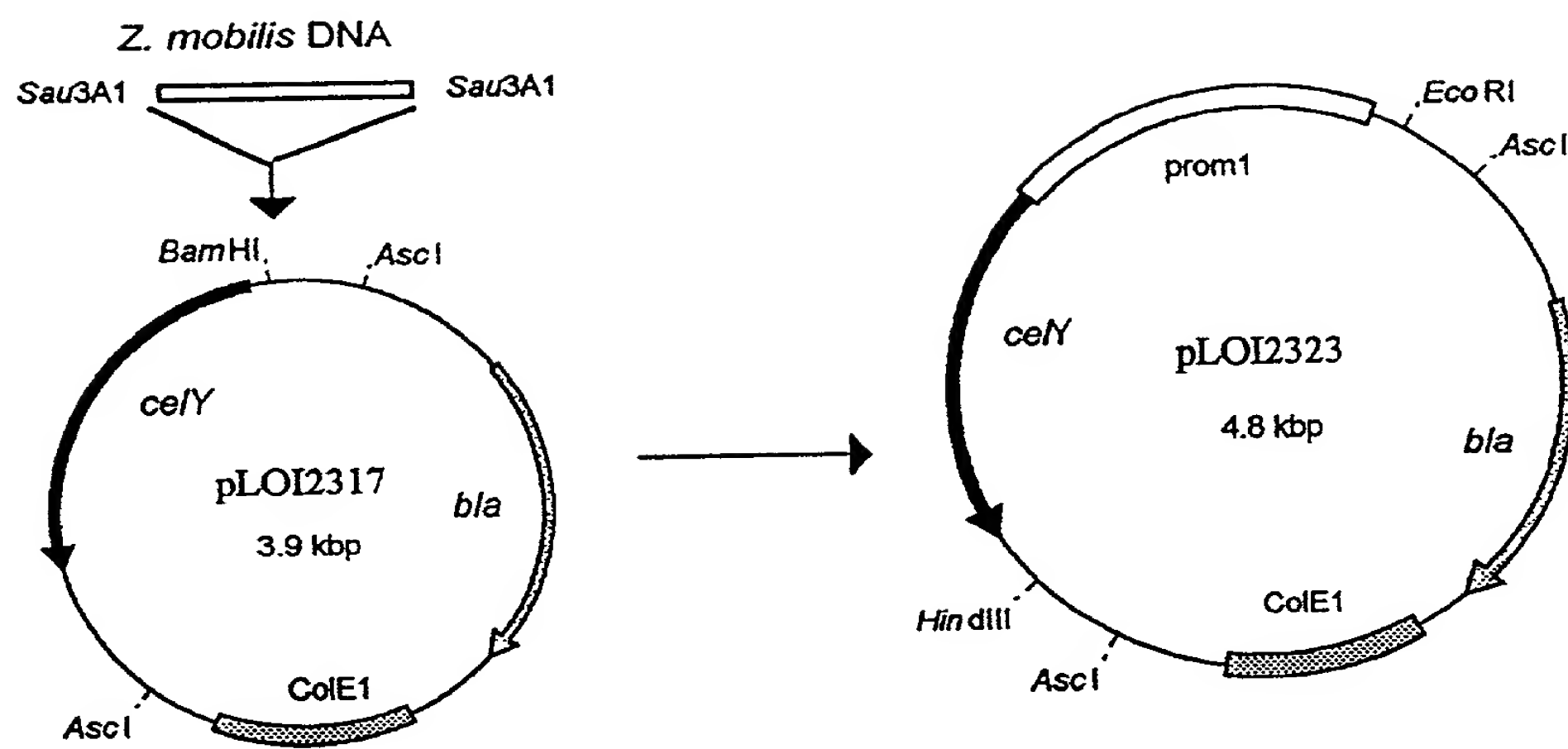
Fig. 14

Position (bp)		RNA Start	Proposed δ factors	δ factor consensus sequence	
-35 ... -10				-35	-10
ATATTTTGATTTTCAAGAAAAAGCCTGATATCTTCCAACATCTT		T (2)	δ^{70}	TTGACA	TATAAT
GATTTGATCCTCTAGAGTCAACCTGCTTGTTACTCGTGATCCCAT		A (4)	δ^{70}	TTGACA	TATAAT
GAGTCAACCTGCTTGTTACTCGTGATCCCATTCACAAGGGCGAA		C (1)	δ^{32}	CTTGAAA	CCCCAT
TTACTCGTGATCCCATTCACAAGGGGCGAATTAATTCGCCCTT		C (3)	δ^{38}	CCGCCT	TATACT

¹Transcriptional starts for *celY* were identified by primer extension analysis. Four promoters were identified. Upstream sequence of these promoters with similarity to *E. coli* -35 and -10 regions are marked with underlines. RNA start sites are bolded. Putative promoters are numbered in parenthesis adjacent to the start site in decending order from the strongest. Differences in intensities were small, within 2-fold.
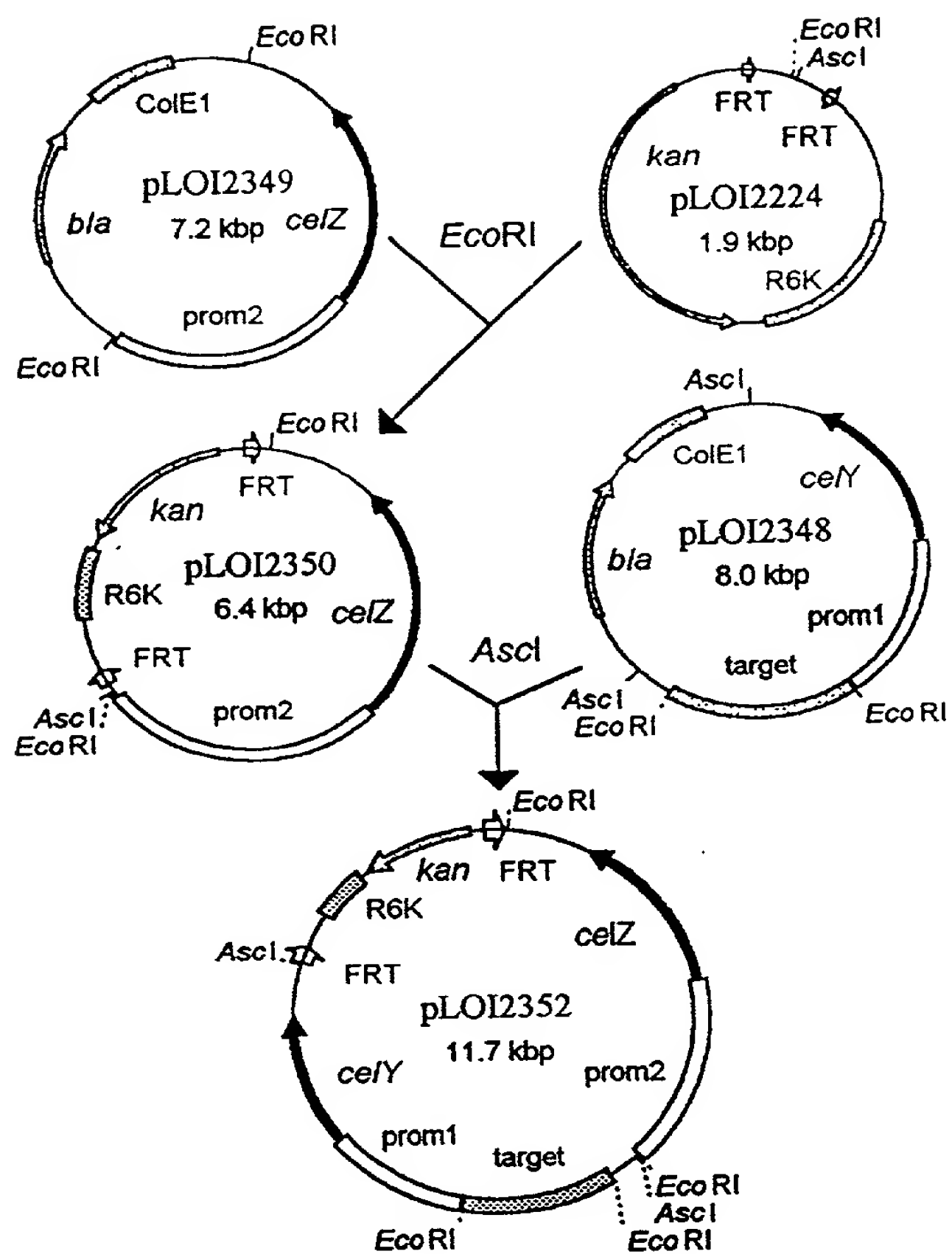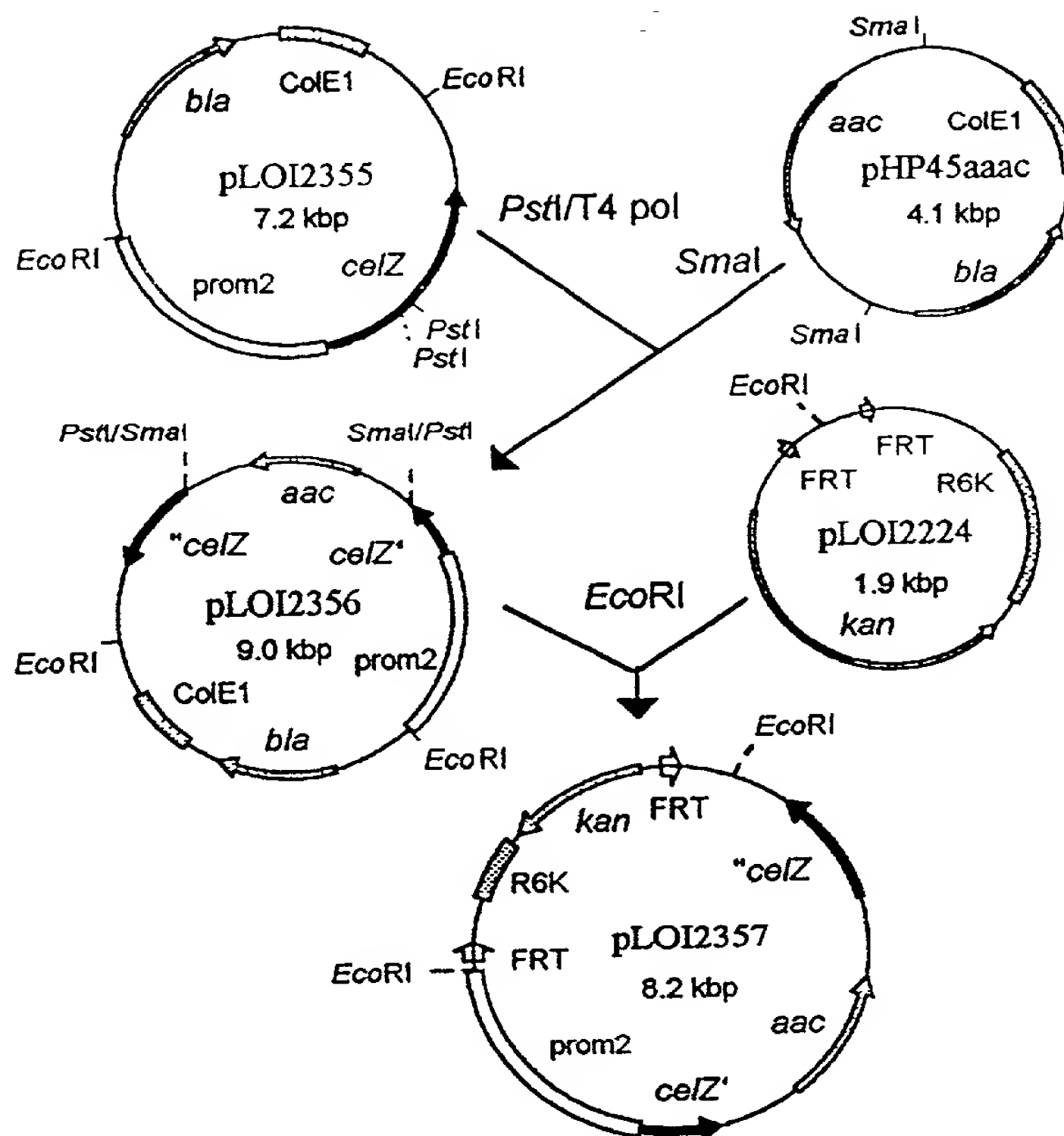
Fig. 15

Fig. 16

Fig. 17

A	B
K. oxytoca P2 (pCPP2006) No endoglucanase	*K. oxytoca* SZ21 (pCPP2006) CelY and CelZ

G1

G2

G3

G4
G5
G6

G7+

0 h   10 h   36 h   0 h   10 h   36 h
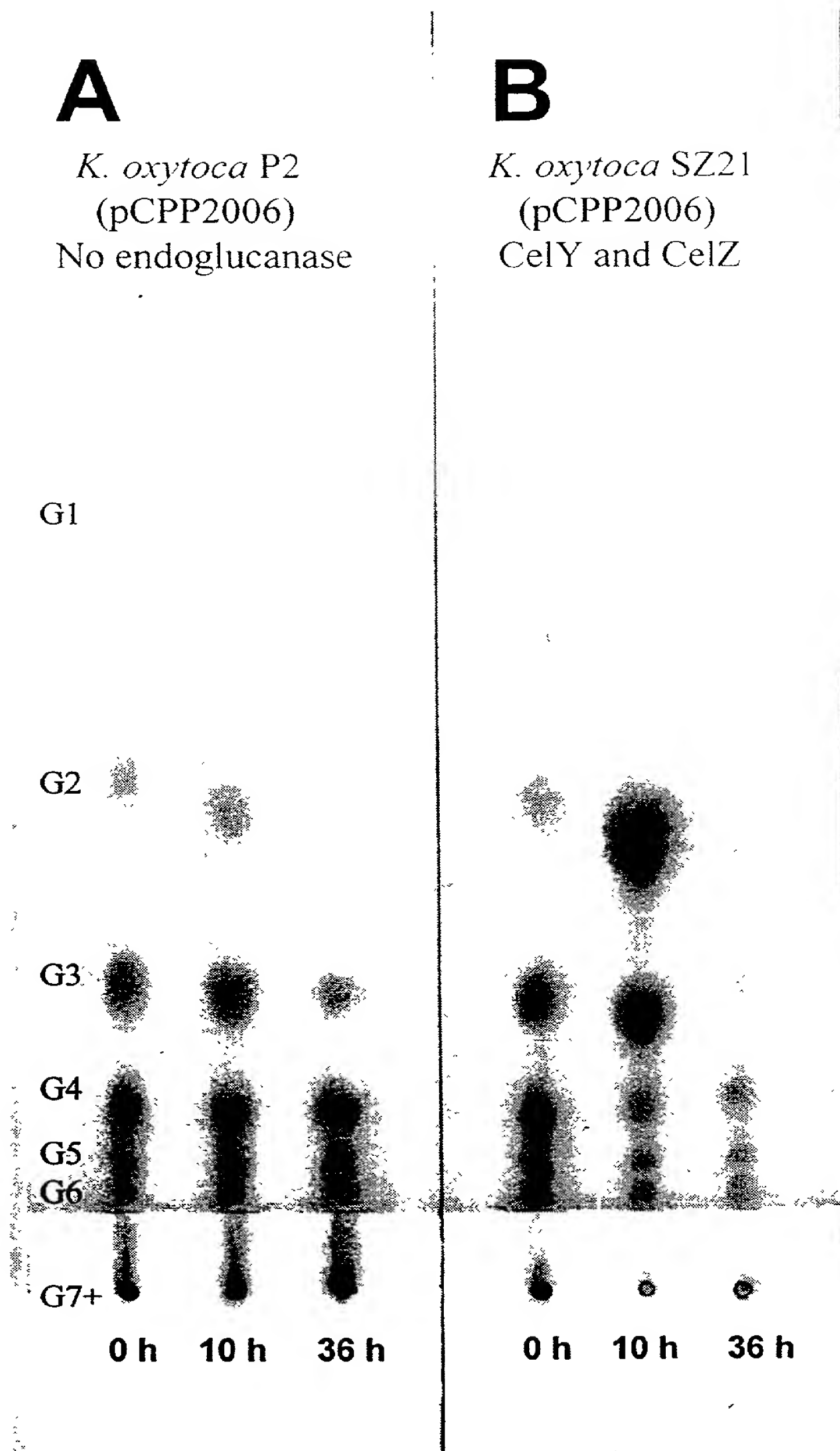
Fig. 18